

The list of best scores is:

Sequence Name	Description	Length	Init. Score	Opt. Sig.	Frame
1. aa502552	TOIG of: aa502552	check: 644	311	161	208
2. a1247782	TOIG of: a1247782	check: 654	354	117	-0.71
					0

1. US-09-765-231A-58 (1-225)

aa502552 TOIG of: aa502552 check: 4648 from: 1 to: 341

LOG 01: A830255Z CHECK: 4648 FROM: 1 TO: 34]

LOCUS	AA502552	341 bp	mRNA	linear	EST 19-AUG-1997
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sequence.
AA502552

KEYWORDS: EST, AAC302352.1, GI:2237519

ORGANISM	Homo sapiens
Source	Human

Mammalia; Eutheria; Primates; Catarrhini; Hominoidea: HOMO

AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>

Tumor Gene Index
TTPBNT
TTPBNT

COMMENT
Contact: Robert Strausberg, Ph.D
Email: cgarbhs-r@mail.nih.gov

Issue Procurement: L. Jeffrey Medeiros, M.D., Michael R. Emmert-Buck, M.D., Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

Clone distribution: NCI-CGAP clone distribution information can be

www-bio.11n1.gov/bbrp/image/image.html

seq primer: -40m13 fwd. ET from Amersham
High quality sequence store: 310

Source

`/db_xref="taxon:9606"`

/clone_11b="NCI_CGAP_L1p2"

```
/lab_host="DH10B"
```

made by oligo-dT priming. Non-directionally cloned, size-selected cDNA fragments were ligated into the

reference: Kizman et al. (1996) Cancer Research
56:5380-5383.

[illegible]

AA502552 Length: 341 October 1, 2002 12:36 Type: N Check: 4648

Initial Score	-	161	Optimized Score	-	208	Significance	-	0.71
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gaps - 1 Conservative Substitutions - 0

	10	20	30	40	50	60	70
TGATGGTAAGTGTCTTCAGGCATTAAATTTCGAATAAATTATCACCACCACTCATCCACTC							

GGTCGACGGCATAAATTGAAATAATTATGAGGCTCCATGAMATGCTATATTCCTTTT

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CCCTCAGAGAATATTTAGTTTCACTCAGGTTTCAAGCTACGCTGTCCCCCAAAACGAACAAAC-

CCCTCAGAGATATTAGTTTCAAGCTACGCTGTCCCAAAACGAACAAACA
70 80 90 100 110

